Lysyl oxidase

Lysyl oxidase (LOX), also known as protein-lysine 6-oxidase, is an enzyme that, in humans, is encoded by the LOX gene.

It catalyzes the conversion of lysine molecules into highly reactive aldehydes that form cross-links in extracellular matrix proteins. Its inhibition can cause osteolathyrism, but, at the same time, its upregulation by tumor cells may promote metastasis of the existing tumor, causing it to become malignant and cancerous.

Results demonstrated that high levels of LOXs expressions were positively associated with glioma grades, older age and MGMT unmethylated status while elevations of LOXs were negatively correlated with IDH mutation or 1p/19q co-deletion. Furthermore, the glioma patients with low levels of LOXs also exhibited better prognosis. Also, differential LOXs expressions were associated with at least 12 chemotherapeutic drug sensitivity. Besides, it was also found that glioma patients with high LOXs expressions showed higher enrichment scores for immune cell infiltration and increased levels of immune checkpoints, suggesting the critical role of distinct LOXs expression levels for glioma immunotherapy. The predictive roles of LOXs expression in tumor immunotherapy were also validated in two immunotherapy cohorts including IMvigor 210 and Van Allen 2015. Experimental results revealed that expressions of LOX, LOXL1, LOXL2, and LOXL3 were higher in glioma cell lines at mRNA and protein levels. The findings altogether indicate that LOXs have potent predictive value for prognosis, chemotherapy and immunotherapy in glioma patients [1].

Lysyl oxidase (LOX) controls the cross-linking and maturation of elastin and collagen fibers. In this study, we investigated the association between LOX gene polymorphisms and intracranial aneurysm (IA) formation in a homogeneous Korean population. MATERIALS AND METHODS:

This cross-sectional study involved 80 age-sex matched patients with IA and controls. Fisher's exact test was performed to analyze allelic associations between ten single nucleotide polymorphisms (SNPs) and IA, including 41 ruptured and 39 unruptured cases. Haplotype-specific associations were analyzed using the omnibus test estimating asymptotic chi-square statistics.

Of ten SNPs, three SNPs (rs2303656, rs3900446, and rs763497) were significantly associated with IA ($p<0.01$). The C allele of rs3900446 was significantly related to increased IA risk with a significant threshold [odds ratio (OR)=20.15, $p=4.8\times10^{-5}$]. Meanwhile, the A allele of rs2303656 showed a preventive effect against IA formation ($p=8.2\times10^{-4}$). Seventeen of 247 haplotype structures showed a suggestive association with IA (asymptotic $p<0.001$). Of ten SNP haplotype combinations, the CG combination of rs3900446 and rs763497 reached Bonferroni-adjusted significant threshold in IA patients (minor haplotype frequency=0.113, asymptotic $p=1.3\times10^{-5}$). However, there was no association between aneurysm rupture and the LOX gene.

This preliminary study indicated that LOX gene polymorphisms, such as rs2303656, rs3900446, and rs763497, may play crucial roles in IA formation in the Korean population. Our novel findings need to be validated in a large-scale independent population [2].

1)

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predictions of prognosis, chemotherapy and immunotherapy in glioma. Front Pharmacol. 2022 Aug 31;13:990461. doi: 10.3389/fphar.2022.990461. PMID: 36160460; PMCID: PMC9490755.

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